

GenCore version 5.1.1.8
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OM protein - protein search, using sw model
Run on: May 20, 2006, 20:19:26 ; Search time 298 Seconds
(without alignments)
450.091 Million Cell updates/sec
Title: US-10-705-716A-2
Perfect score: 767
Sequence: 1 MCGGSRADALEPRYESTWT.....VTENIRQMDRSKRVTKNCIN 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2849598 seqs, 92501592 residues
Total number of hits satisfying chosen parameters: 2849598
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Uniprot_7.2.1*
1: uniprot_eprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	767	100.0	145	Q920K5	RAT
2	746	97.3	145	Q8VHV1	MUS
3	645	84.1	145	Q9HA93	HUMAN
4	634	82.7	145	Q8WNE9	PIG
5	617.5	80.5	180	Q8WXS3	HUMAN
6	473.5	61.7	149	Q8WXS1	HUMAN
7	459	59.8	123	Q9CYS9	MOUSE
8	294	38.3	54	Q790N3	RAT
9	294	38.3	54	Q8VBS8	MOUSE
10	288	37.5	73	Q8WXS0	HUMAN
11	278	36.2	54	Q8WTP6	HUMAN
12	272	35.5	80	Q8WXS2	HUMAN
13	267	34.8	54	Q8WNE8	PIG
14	166.5	21.7	51	Q4RR60	TETNG
15	161	21.0	32	Q801V5	BRARE
16	160.5	20.9	36	Q4S712	TETNG
17	92.5	12.1	613	Q6ZMJ6	HUMAN
18	92.5	12.1	753	CNOT3	HUMAN
19	92.5	12.1	1073	PVDA	FLAKN
20	89.5	11.7	177	Q4Q487	LEISHA
21	89	11.6	281	Q3W1F9	9ACTO
22	88	11.5	365	POLG	SUMUS
23	87	11.3	1035	Q76C74	YEAST
24	87	11.3	1713	Q8TGE1	YEAST
25	86.5	11.3	397	Q4DTZ6	TRYCR
26	86.5	11.3	554	Q4HWN0	GIBBERA
27	86.5	11.3	1195	Q5BBD7	EMENI
28	86	11.2	585	Q7UZ29	RHOBA
29	86	11.2	1070	PVDZ29	FLAKN
30	86	11.2	1894	Q4Q515	LEISHA
31	85.5	11.1	733	Q4QGH8	LEISHA

32	85	11.1	450	2	Q9QLT5	ORYSA
33	85	11.1	507	2	Q4LTE7	9BURK
34	85	11.1	932	2	Q3F8F8	9BURK
35	84.5	11.0	534	2	Q96SA2	HUMAN
36	84	11.0	155	2	Q6USP5	PLAFA
37	84	11.0	408	2	Q4D6E3	TRYCR
38	83.5	10.9	214	2	Q8WTC3	LEUMA
39	83.5	10.9	341	2	Q3IMK3	SYNP7
40	83.5	10.9	341	2	Q5MZC6	SYNP6
41	83.5	10.9	677	2	Q6A015	MOUSE
42	83.5	10.9	700	2	Q30678	XANMA
43	83.5	10.9	751	1	CNOT3	MOUSE
44	83.5	10.9	953	1	Q5BATS	EMENI
45	83	10.8	314	2	Q5BEH2	EMENI

ALIGNMENTS

RESULT 1
Q920K5 RAT
ID Q920K5 RAT PRELIMINARY; PRT; 145 AA.
AC Q920K5
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Dem-A20-4 (BAALC isoform 1-6-8).
GN Name=dem-A20-4; Synonyms=BaalC;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1559234; DOI=10.1111/j.1471-4159.2004.02902.x;
RA Wang X., Tian Q.B., Okano A., Sakagami H., Moon I.S., Kondo H.,
RA Endo S., Suzuki T.;
RT "BAALC 1-6-8 protein is targeted to postsynaptic lipid rafts by its N-terminal miristoylation and palmitoylation, and interacts with a, but not b, subunit of Ca2+/calmodulin-dependent protein kinase II.";
RL J. Neurochem. 92:647-659(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Spague-Dawley;
RC MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plasas C., Heinson K.,
RA Mrozek K., Sill H., Khutilla S., Koltz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de La Chapelle A.,
RT "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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CC EMBL; AB073318; BAB70507.1; -; mRNA.
DR EMBL; AF3171321; AAL50517.1; -; mRNA.
DR Ensembl; ENSRNOG00000004697; Rattus norvegicus.
DR RGD; 628703; BaalC.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
SQ SEQUENCE 145 AA; 15475 MW; D5A27AD67456F341 CRC64;

Query Match 100.0%; Score 767; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCGGSRADALEPRYESTWTETSTWLTYSALPSAAATDSGPEAGLHAGVLEDPG 60
DB 1 MCGGSRADALEPRYESTWTETSTWLTYSALPSAAATDSGPEAGLHAGVLEDPG 60
QY 61 SSGVLRPAAPGGIANPEKKNMCGTCPCNSQSLSSGPLTQKQNGLWTTTEAKRDAKMSAR 120


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RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AK022077; BAB13960.1; -; mRNA.
DR EMBL; AF371319; AAL50515.1; -; mRNA.
DR EMBL; BC011517; AAL11517.1; -; mRNA.
DR EMBL; AF363578; AAL50377.1; -; Genomic DNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N.1.
DR SRA; SRR111111.1; BAALC_N.1.
SQ SEQUENCE 145 AA; 15551 MW; C75ED7D00BF92E26 CRC64;

Query Match 84.1%; Score 645; DB 2; Length 145;
Best Local Similarity 83.4%; Pred. No. 7.9e-50;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MCGGSRADAEIPRYESWTRETESTWLTYYTDSALPSAAATDSGPAGGLHAGVLEDGP 60
DB 1 MCGGSRADAEIPRYESWTRETESTWLTYYTDSALPSAAATDSGPAGGLHAGVLEDGP 60

QY 61 SSSGVLPAAPGGIANPEKKNCGTCQPNQSLSGGPLTKQNGLWTEAKRDKRMSAR 120
DB 61 PSNGVPRSTAGGTPNPKKTCNCTQCPNPSLSGGPLTKQNGLWTEAKRDKRMPAK 120

QY 121 EVASVTENIRQMDRSKRVTKNCIN 145
DB 121 EVTINVTDISIQQMDRSRRTKNCYN 145

RESULT 4
Q8WNE9_PIG PRELIMINARY; PRT; 145 AA.
AC Q8WNE9;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE BAALC isoform 1-6-8.
GN Name=BAALC;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub.
OX NCBI_TaxID=9823;
SQ SEQUENCE 145 AA; 15551 MW; C75ED7D00BF92E26 CRC64;

Query Match 80.5%; Score 617.5; DB 2; Length 180;
Best Local Similarity 67.2%; Pred. No. 3e-47;
Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;

QY 1 MCGGSRADAEIPRYESWTRETESTWLTYYTDSALPSAAATDSGPAGGLHAGVLEDGP 60
DB 1 MCGGSRADAEIPRYESWTRETESTWLTYYTDSALPSAAATDSGPAGGLHAGVLEDGP 60

QY 54 -----GVLEDPSSNGVLPRPAAPGGIANPEKKNCGT 85
DB 61 KIKAPTDVSDEGLPSAKMAPLAVFSGHMGLEDGLPSNGVPRSTAGGTPNPKKTCNCT 120

QY 86 QCPNSQSLSSGGLTKQNGLWTEAKRDKRMSAREVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 QCPNPSLSGGPLTKQNGLWTEAKRDKRMPAKEVTINVTDISIQQMDRSRRTKNCYN 180

RESULT 6
Q8WXS1_HUMAN PRELIMINARY; PRT; 149 AA.
ID Q8WXS1;
AC Q8WXS1;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE BAALC 1-5-6-8.
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de La Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
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CC -----
DR EMBL; AF363578; AAL50379.1; -; Genomic DNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR HGNC; HGNC:14333; BAALC.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N.1.
SQ SEQUENCE 180 AA; 19224 MW; 380183E0F188F684 CRC64;

Query Match 80.5%; Score 617.5; DB 2; Length 180;
Best Local Similarity 67.2%; Pred. No. 3e-47;
Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;

QY 1 MCGGSRADAEIPRYESWTRETESTWLTYYTDSALPSAAATDSGPAGGLHAGVLEDGP 60
DB 1 MCGGSRADAEIPRYESWTRETESTWLTYYTDSALPSAAATDSGPAGGLHAGVLEDGP 60

QY 54 -----GVLEDPSSNGVLPRPAAPGGIANPEKKNCGT 85
DB 61 KIKAPTDVSDEGLPSAKMAPLAVFSGHMGLEDGLPSNGVPRSTAGGTPNPKKTCNCT 120

QY 86 QCPNSQSLSSGGLTKQNGLWTEAKRDKRMSAREVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 QCPNPSLSGGPLTKQNGLWTEAKRDKRMPAKEVTINVTDISIQQMDRSRRTKNCYN 180

RESULT 6
Q8WXS1_HUMAN PRELIMINARY; PRT; 149 AA.
ID Q8WXS1;
AC Q8WXS1;
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DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE BAALC 1-5-6-7-8.
 GN Name=BAALC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
 RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Archer C., Heinonen K.,
 RA Mrozek K., Sill H., Knuutila S., Koltz J.B., Archer K.J.,
 RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
 RT "BAALC, the human member of a novel mammalian neuroectoderm gene
 RT lineage, is implicated in hematopoiesis and acute leukemia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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 CC -----
 DR EMBL; AF363578; AAL50381.1; -; Genomic DNA.
 DR Ensembl; ENSG00000164929; Homo sapiens.
 DR InterPro; IPR009728; BAALC.N.
 DR Pfam; PF06989; BAALC.N; 1.
 SQ SEQUENCE 149 AA; 15577 MW; DB26C19969B91P6E CRC64;

 Query Match 61.7%; Score 473.5; DB 2; Length 149;
 Best Local Similarity 66.0%; Pred. No. 1.9e-34;
 Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;

 QY 1 MCGGSRADAIPRYESWTRETESTWLTWYDSDALPSAAATDSCPEAGGLHA----- 53
 DB 1 MCGGSRADAIPRYESWTRETESTWLTWYDSDALPSAAATDSCPEAGGLHVLAEKKS 60

 QY 54 -----GVLEDPSSGVNLPRAPAGGIANPEKKKNGCT 85
 DB 61 KIKAPTDSVDEGLFSASQWAPLAFVSHGMLDGLPSGVPRSTAPGGIPNPEKTKNCT 120

 QY 86 QCPNSQSLSSGLTKQKGLWTTTE 109
 DB 121 QCPNPQSLSSGLTKQKGLQTTE 144

 RESULT 7
 Q9CYS9_MOUSE PRELIMINARY; PRT; 123 AA.
 ID Q9CYS9_MOUSE
 AC Q9CYS9;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE 10, 11 days embryo whole body cDNA, RIKEN full-length enriched
 DE library, clone:2810457D07 product:brain and acute leukemia,
 DE cytoplasmic, full insert sequence.
 GN Name=BaalC;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1016/S0076-6879(99)03004-9;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=whole body;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Banaal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Keiso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuura H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Fabriz S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibusata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
 RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanihi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=whole body;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=whole body;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nitaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirali L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
 RA Kanai A., Kawai H., Kawasaki Y., Kedzierski R.M., King B.L.,
 RA Kagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OX Muroidea; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12986/SVETac;
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Koltz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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CC -----
DR EMBL; AF371324; AAL50520.1; -; mRNA.
DR Ensembl; ENSMUSG00000063057; Mus musculus.
DR MGI; MGI:1928704; BaalC.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
SQ SEQUENCE 54 AA; 5667 MW; FEE8C0E9BFCDB829 CRC64;

Query Match 38.3%; Score 294; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 7.2e-19;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIPRYESWTRETESTWLTYYTSDALPSAAATDSDGPEAGLHAG 54
Db 1 MCGGSRADAIPRYESWTRETESTWLTYYTSDALPSAAATDSDGPEAGLHAG 54

RESULT 10
QWXS0 HUMAN
ID QWXS0 HUMAN PRELIMINARY; PRT; 73 AA.
AC QWXS0;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE BAALC 1-4-5-6-8.
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Koltz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
CC -----
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CC -----
DR EMBL; AF371323; AAL50519.1; -; mRNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
SQ SEQUENCE 73 AA; 7871 MW; 98DBC286E8F524A CRC64;

Query Match 37.5%; Score 288; DB 2; Length 73;
Best Local Similarity 91.4%; Pred. No. 3.5e-18;
Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIPRYESWTRETESTWLTYYTSDALPSAAATDSDGPEAGLHAGVIED 58

Db 1 MCGGSRADAIPRYESWTRETESTWLTYYTSDALPSAAATDSDGPEAGLHAGVIED 58
RESULT 11
QWTP6 HUMAN
ID QWTP6 HUMAN PRELIMINARY; PRT; 54 AA.
AC QWTP6;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE BAALC isoform 1-8 (Brain and acute leukemia, cytoplasmic, isoform 2)
DE (BAALC 1-8).
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Koltz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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CC -----
DR EMBL; AF371323; AAL50519.1; -; mRNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
SQ SEQUENCE 54 AA; 5663 MW; FEF0B4EABED9B829 CRC64;

Query Match 36.2%; Score 278; DB 2; Length 54;
Best Local Similarity 94.4%; Pred. No. 2e-17;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIPRYESWTRETESTWLTYYTSDALPSAAATDSDGPEAGLHAGVIED 58

Qy 1 MGCGSRADAI EPRYYESWTR ETSTWLTYTSDALPSAAATDSGEAGGLHAG 54
Dd 1 MGCGSRADAI EPRYYESWTR ETSTWLTYTSDAPPSSAAPDPSGEAGGLHSG 54	


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RESULT 15
QB01V5_BRARB PRELIMINARY; PRT; 32 AA.
AC QB01V5;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Novel protein similar to human brain and acute leukemia, cytoplasmic
DE (BAALC) (Fragment).
GN Name=baalc; Synonyms=OTTDPAR0000001859; ORFNames=ZC215113.3-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sehra H.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AL807244; CAD87801.1; -; Genomic_DNA.
DR ZFIN; ZDB-GENE-030616-613; baalc.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
FT NON_TER 32
FT 32
SQ SEQUENCE 32 AA; 3663 MW; 916A5445D263B7F7 CRC64;

Query Match 21.0%; Score 161; DB 2; Length 32;
Best Local Similarity 90.6%; Pred. No. 3.3e-07;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGGSRADAIEPRYVESWTRETESTLTNTD 32
Db |||||
1 MCGGSRADAIEPRYQESWTRETESTLTNTD 32

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Search completed: May 20, 2006, 20:26:16
Job time : 301 secs

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